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============================================================
Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2008; month=3; day=18; hr=17; min=39; sec=41; ms=23; ]
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Application No: 10573229   Version No: 2.1

                    Input Set:

                    Output Set:

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                   Finished: 2008-03-18 17:38:16.531
                    Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 707 ms
            Total Warnings: 134
              Total Errors: 0
      No. of SeqIDs Defined: 312
         Actual SeqID Count: 312

Error code   Error Description

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W   213   Artificial or Unknown found in <213> in SEQ ID (4)

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W   213   Artificial or Unknown found in <213> in SEQ ID (8)

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W   213   Artificial or Unknown found in <213> in SEQ ID (12)

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W   213   Artificial or Unknown found in <213> in SEQ ID (16)

W   213   Artificial or Unknown found in <213> in SEQ ID (19)

W   213   Artificial or Unknown found in <213> in SEQ ID (20)

W   213   Artificial or Unknown found in <213> in SEQ ID (23)

W   213   Artificial or Unknown found in <213> in SEQ ID (24)

W   213   Artificial or Unknown found in <213> in SEQ ID (27)

W   213   Artificial or Unknown found in <213> in SEQ ID (28)

W   213   Artificial or Unknown found in <213> in SEQ ID (31)

W   213   Artificial or Unknown found in <213> in SEQ ID (32)

W   213   Artificial or Unknown found in <213> in SEQ ID (35)

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        Input Set:


        Output Set:



          Started:   2008-03-18 17:38:08.824
         Finished:   2008-03-18 17:38:16.531
          Elapsed:   0 hr(s) 0 min(s) 7 sec(s) 707 ms
   Total Warnings:   134
     Total Errors:   0
No. of SeqIDs Defined:   312
   Actual SeqID Count:   312
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Error code   Error Description

      This error has occured more than 20 times, will not be displayed

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tgagccactt tggaagctga tcttggagca ccagtcaagc ccttagctgg ctgcagccac   180

agccaacaac aagactgcaa cctcctgggg gatcctgagc cagaatcccc tggctaaatt   240

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atcattgctt ctgctgggcg actgagaagc atcacccact ccccagaac cttttttacg   420

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gagagacctc taaccctggg agaggaggga gggaaatctc gaggaccag ggttatgcaa   660

caacacaagg gaagtacctg ctgggttctg ggggttgggg aaggaaaatc cctactgccc   720

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<210>   2
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<212>   PRT
<213>   Homo sapiens

<400>   2

Arg Arg Phe Leu Trp Gly Phe Lys Gly Phe Ser Leu Arg Arg Leu Gly
1   5   10   15

Lys Ile Pro Leu Gly Phe Phe Pro Pro Pro Leu Gly Gly Lys Ala Leu
            20   25   30

Thr Pro Gly Glu Ala Gly Lys Ala Pro Leu Phe Gln Gly Phe Arg Ala
        35   40   45

Pro Pro Gly Pro Gly Ala Ser Ile Ser Cys Ala Leu Gly Ser Gly Leu
    50   55   60

Ala Leu Gly Ala Val Gly Ile Phe Leu Pro Gln Pro Pro Glu Pro Ser
65   70   75   80

Arg Tyr Phe Pro Cys Val Val Ala
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<213>   Artificial Sequence

<220>
<223>   Oligonucleotide

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<220>

<223> Oligonucleotide

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<211> 2856
<212> DNA
<213> Homo sapiens

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ttcttcctga gccaccttgc tttcctggat gcctgctgtg cctcagtaat cacccctcag   240

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ttctctttct tcaccatatg tgcaggcaca gagtgttacc tgctgtcagt gatggcctat   360

gaccgctttg ttgccattag caatccactg cactgtaaca tgaccatgac tccaggtacc   420

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gccattgttg acactttga cttcagagca ccttctggaa aagagcttct gttggatgac      2220

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aagaccacac agcacctctc acatcccaag ctccaggagt cccttcctct gtctgcaacg      2340

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aaagccttcc ctgacccaga agagaaatcg caatgtcacc agtttctctt tctcccttca      2460

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<210>  6
<211>  951
<212>  PRT
<213>  Homo sapiens
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Phe Thr Asp His Pro Glu Leu Ala Val Pro Leu Phe Leu Val Phe Leu
            20   25   30

Ser Phe Tyr Leu Val Thr Phe Leu Gly Asn Gly Gly Met Ile Ile Leu
        35   40   45

Ile Gln Val Asp Ala Gln Leu His Thr Pro Val Tyr Phe Phe Leu Ser
    50   55   60

His Leu Ala Phe Leu Asp Ala Cys Cys Ala Ser Val Ile Thr Pro Gln
65   70   75   80

Ile Leu Ala Thr Leu Ala Thr Asp Lys Thr Val Ile Ser Tyr Gly Cys
                85   90   95

Arg Ala Val Gln Phe Ser Phe Phe Thr Ile Cys Ala Gly Thr Glu Cys
            100   105   110

Tyr Leu Leu Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Ser Asn
        115   120   125

Pro Leu His Cys Asn Met Thr Met Thr Pro Gly Thr Cys Arg Val Phe
    130   135   140

Leu Ala Ser Ala Phe Ile Cys Gly Val Ser Gly Ala Ile Leu His Thr
145   150   155   160

Thr Cys Thr Phe Thr Leu Ser Phe Cys Cys Asp Asn Gln Ile Asn Phe
            165   170   175

Phe Phe Cys Asp Leu Pro Pro Leu Leu Lys Leu Ala Cys Ser Ser Met
            180   185   190

Thr Gln Thr Glu Ile Val Ile Leu Leu Cys Ala Lys Cys Met Phe Leu
        195   200   205

Ala Asn Val Met Val Ile Leu Ile Cys Tyr Met Leu Ile Ile Arg Ala
    210   215   220

Ile Leu Arg Val Lys Ser Ala Gly Gly Leu Leu Ile Ala Ser Ala His
225   230   235   240

Phe Asp Ala Tyr Val Tyr Glu Thr Gly Ile Asn Tyr Asn Thr Val Tyr
                245   250   255

Gly Ser Gly Lys Ala Val Gly Trp Ser Trp Arg Ser Leu Arg Glu Thr
                260   265   270

Asn His Met Arg Pro Gly Asn Thr Ser Lys His Ser Ala Ala Gln Leu
            275   280   285

His Gln Cys Leu Ile Gln Gln Val Gly Arg Trp Pro Leu Gln Ser Met
            290   295   300

Pro Phe Pro Val Ser Ala Gly Pro Pro Tyr Lys Ser Val Gln Pro Leu
305   310   315   320

Pro Gly Asp Pro Arg Pro Leu Leu Cys Ile Thr Gly Leu Phe Leu Thr
                325   330   335

Leu Lys Met Met Gly Cys Gly Pro Arg Arg Pro Arg Asp Arg Lys Ser
            340   345   350

Asp Phe Phe Ile Asn Thr Asp Pro Gly Ala Gly Ser Pro Glu Glu Gln
            355   360   365

Arg Cys Gly Trp Glu Gly His Pro Ser His Ser Tyr Thr Leu Gly Leu
    370   375   380

Ser Leu Pro Val Asn Phe Gly Leu Lys Cys Pro Trp Trp Thr Leu Ser
385   390   395   400

Gly Pro Pro Ala Thr Cys Gln Arg Pro Asp Leu Gln Thr Pro Ser Pro
                405   410   415

Pro Lys Glu Ile Cys Ser Ser Gly Leu Arg Pro Leu Thr His Ser Ala
            420   425   430

Gly Pro Asp Arg Ser Gln Val Pro Ala Ala Ser Gly Ala Ala Thr Met
    435   440   445

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Leu Thr Lys Gly Leu Pro Asp Ile Thr Val Gly Leu Gln Ile Tyr Asp
    450             455             460

Ser Cys Ile Ser Gly Ile Gln Ala Leu Gly Ser Thr Leu Ala Leu Leu
465             470             475             480

Ser Asn Gln Leu Pro Pro Thr Thr Asn Tyr Ala Cys Gly Ser Gln Gln
                485             490             495

His Leu Leu Gly Val Val Gly Gly Met Thr Phe Leu Glu Ser Glu Pro
        500             505             510

Met Ser Glu Leu Leu Ser Ile Tyr Arg Val Pro Gln Gly Gln Arg Leu
        515             520             525

Thr Lys Asn Phe Glu Val Lys Glu Leu Val Cys Thr Tyr Leu Val Gly
    530             535             540

Gln Leu Pro Tyr Gly Leu Val Ser Tyr Asp Asn Ser Asn Phe Glu Trp
545             550             555             560

Leu Asp Gln Gln Leu Gln Lys Gln Ile Gly Gly Glu Gly Leu Pro Val
            565             570             575

Gly Ala Ala Pro Ser Arg Val Ala Arg Gln Gln Ser Asp Glu Glu Ala
            580             585             590

Val Gly Gly Val Gln Gly Tyr Arg Trp Ser Gly Leu Gly Ala Ser Ile
        595             600             605

Gln Ser Ala Arg Glu Gly Ala Trp His Arg Thr Gly Leu Glu Asn Met
    610             615             620

Thr Thr Ala His Leu Ser Ala Phe Lys Leu Pro Asp Leu Thr Ala Thr
625             630             635             640

Tyr Gln Ala Tyr Leu Ala Ala Lys Ala Leu Trp Val Ala Tyr Gln Asn
            645             650             655

Leu Met Ser Cys Ser Glu Arg Glu Gly Pro Phe Leu Gly Gly Thr Tyr
            660             665             670

Ala Asn Ala Trp Glu Ala Arg Leu Ser Gln Val Asn Phe Thr Thr Lys
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            675                   680                    685


Ala Gln Glu Glu Val Phe Phe Ala Lys Asp Gly Glu Val Leu Thr Thr
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Phe Asp Ile Lys Asn Ile Tyr Val Leu Pro Asp Leu Ser Gly Gln Thr
705               710               715                   720


Ala Ile Val Gly His Phe Asp Phe Arg Ala Pro Ser Gly Lys Glu Leu
            725               730               735


Leu Leu Asp Asp Ser Ala Ile Val Trp Ala Glu Gly Pro Leu Lys Ile
            740               745               750


Arg Ala Glu Arg Thr Leu Arg Thr Lys Thr Thr Gln His Leu Ser His
        755               760               765


Pro Lys Leu Gln Glu Ser Leu Pro Leu Ser Ala Thr Lys Asn Val Leu
        770               775               780


Trp Lys Pro Gly Ser Gln Pro Tyr Leu Arg Ser Gln Asn Ala Ala Thr
785               790               795                   800


Lys Ala Phe Pro Asp Pro Glu Glu Lys Ser Gln Cys His Gln Phe Leu
            805               810               815


Phe Leu Pro Ser Asp Ser Val Ala Cys Gln Lys Cys Ser Asp Asn Gln
            820               825               830


Trp Pro Asn Val Gln Lys Gly Glu Cys Ile Pro Lys Thr Leu Asp Phe
        835               840               845


Leu Phe Tyr His Lys Pro Leu Asp Thr Ala Leu Ala Val Cys Thr Ala
        850               855               860


Leu Leu Phe Leu Leu Ala Leu Ala Ile Leu Gly Ile Phe His Val Val
865               870               875                   880


Cys Ser Cys Val Trp Val Ser Phe Ile Pro Ala His Met His Ala His
            885               890               895


Ser Lys Asp Thr Met Ala Met Glu Val Phe Val Ile Leu Ala Ser Ala
            900               905               910
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Gly Gly Leu Met Ser Ser Leu Phe Phe Ser Lys Cys Tyr Ile Ile Leu
        915   920   925

Leu His Pro Glu Lys Asn Thr Lys Asp Gln Met Phe Gly Arg His His
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Arg Lys Trp Glu Lys Leu Lys
945   950

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<213>   Artificial Sequence

<220>
<223>   Oligonucleotide

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<210>   8
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<212>   DNA
<213>   Artificial Sequence

<220>
<223>   Oligonucleotide

<400>   8
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<210>   9
<211>   543
<212>   DNA
<213>   Homo sapiens

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gaagggagaa gaggccgaag aggaaacatg aacttctatt tactcctagc gagcagcatt   180

ctgtgtgcct tgattgtctt ctggaaatat cgccgctttc agagaaacac tggcgaaatg   240

tcatcaaatt caactgctct tgcactagtg agaccctctt cttctgggtt aattaacagc   300

aatacagaca acaatcttgc agtctacgac ctctctcggg atattttaaa taatttccca   360

cactcaatag ccaggcagaa gcgaatattg gtaaacctca gtatggtgga aaacaagctg   420

gttgaactgg aacatactct acttagcaag ggtttcagag gtgcatcacc tcaccggaaa   480

tccacctaaa agcgtacagg atgtaatgcc agtggtggaa atcattaaag acactttgag   540

tag   543

<210>   10
<211>   113
<212>   PRT
<213>   Homo sapiens

<400>   10

Met Asn Phe Tyr Leu Leu Leu Ala Ser Ser Ile Leu Cys Ala Leu Ile
1   5   10   15

Val Phe Trp Lys Tyr Arg Arg Phe Gln Arg Asn Thr Gly Glu Met Ser
            20   25   30

Ser Asn Ser Thr Ala Leu Ala Leu Val Arg Pro Ser Ser Ser Gly Leu
        35   40   45

Ile Asn Ser Asn Thr Asp Asn Asn Leu Ala Val Tyr Asp Leu Ser Arg
    50   55   60

Asp Ile Leu Asn Asn Phe Pro His Ser Ile Ala Arg Gln Lys Arg Ile
65   70   75   80

Leu Val Asn Leu Ser Met Val Glu Asn Lys Leu Val Glu Leu Glu His
                85   90   95

Thr Leu Leu Ser Lys Gly Phe Arg Gly Ala Ser Pro His Arg Lys Ser
            100   105   110

Thr

<210>   11
<211>   22
<212>   DNA
<213>   Artificial Sequence

<220>
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<210> 12
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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<210> 13
<211> 2761
<212> DNA
<213> Homo sapiens

<400> 13
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ccctgaaacc tgcgaggggc ttccgtccac gtccccagtg gacctaccac ccctccatct   180

gggaaagcag gccacagcag ccggacaaag gaagctcctc agcctctagt cgcctctctg   240

tgcatgcaca tcggtcactg atctcgccta ctggcacaga cgtgtttatc ggccaaactg   300

ac